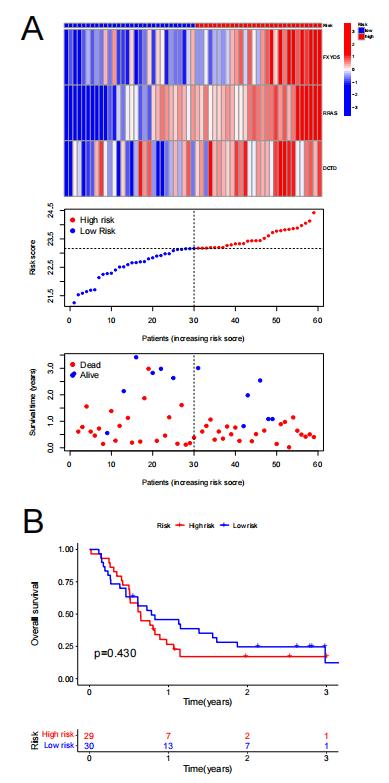
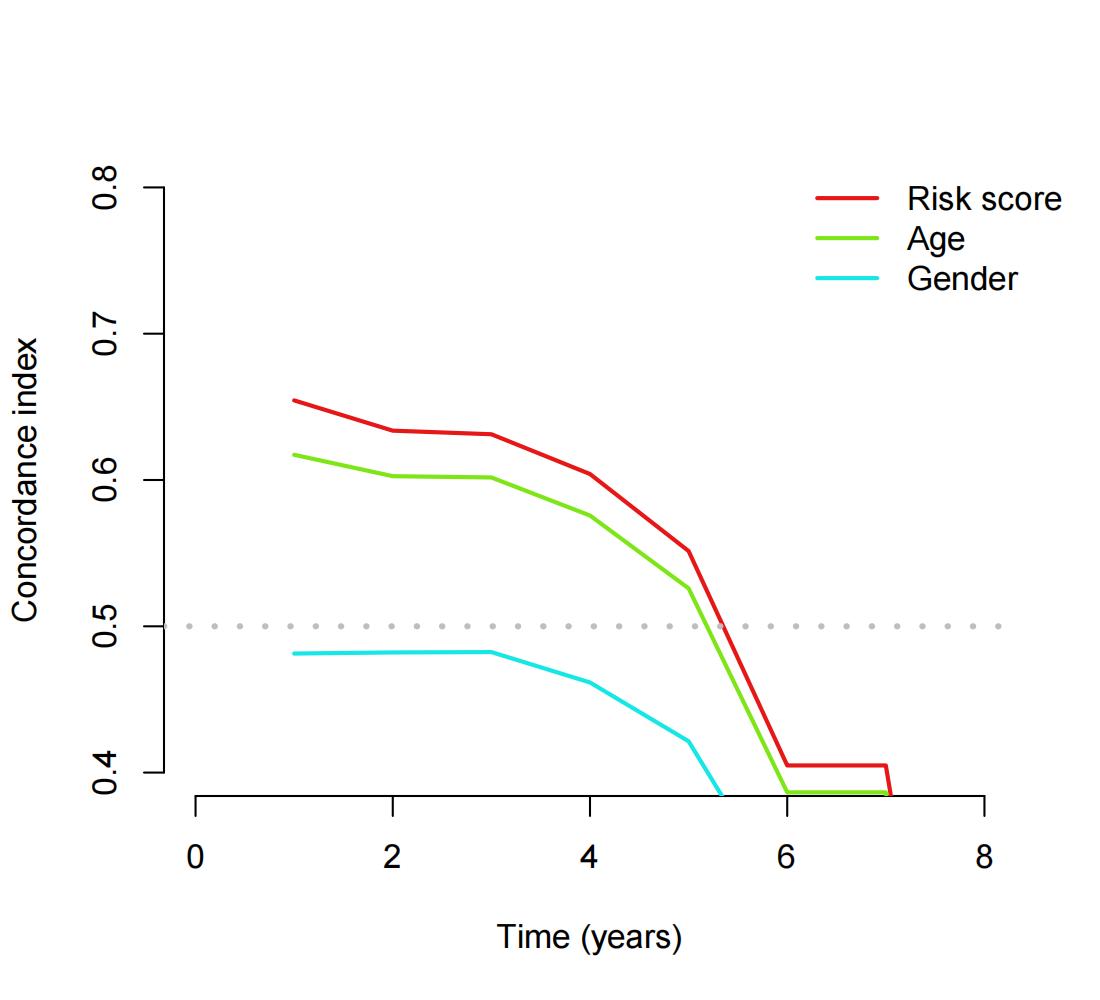
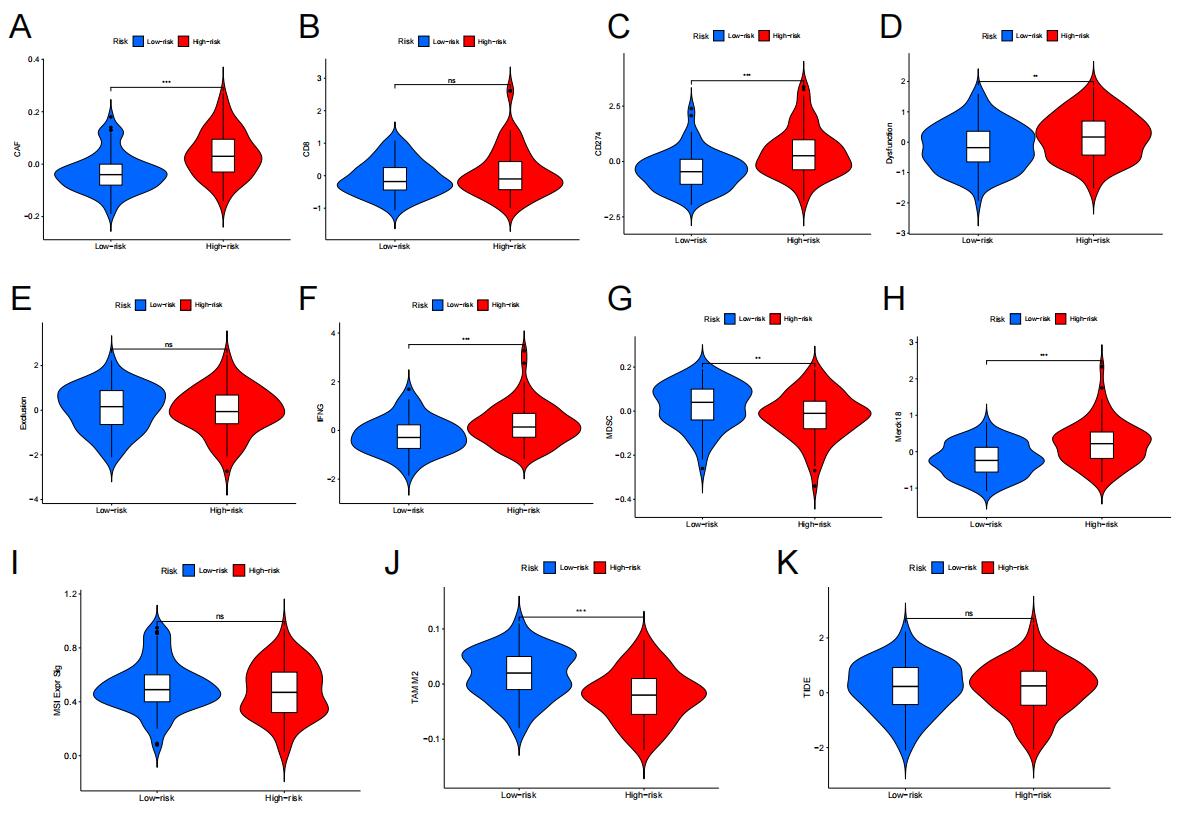
**Supplementary Figs**

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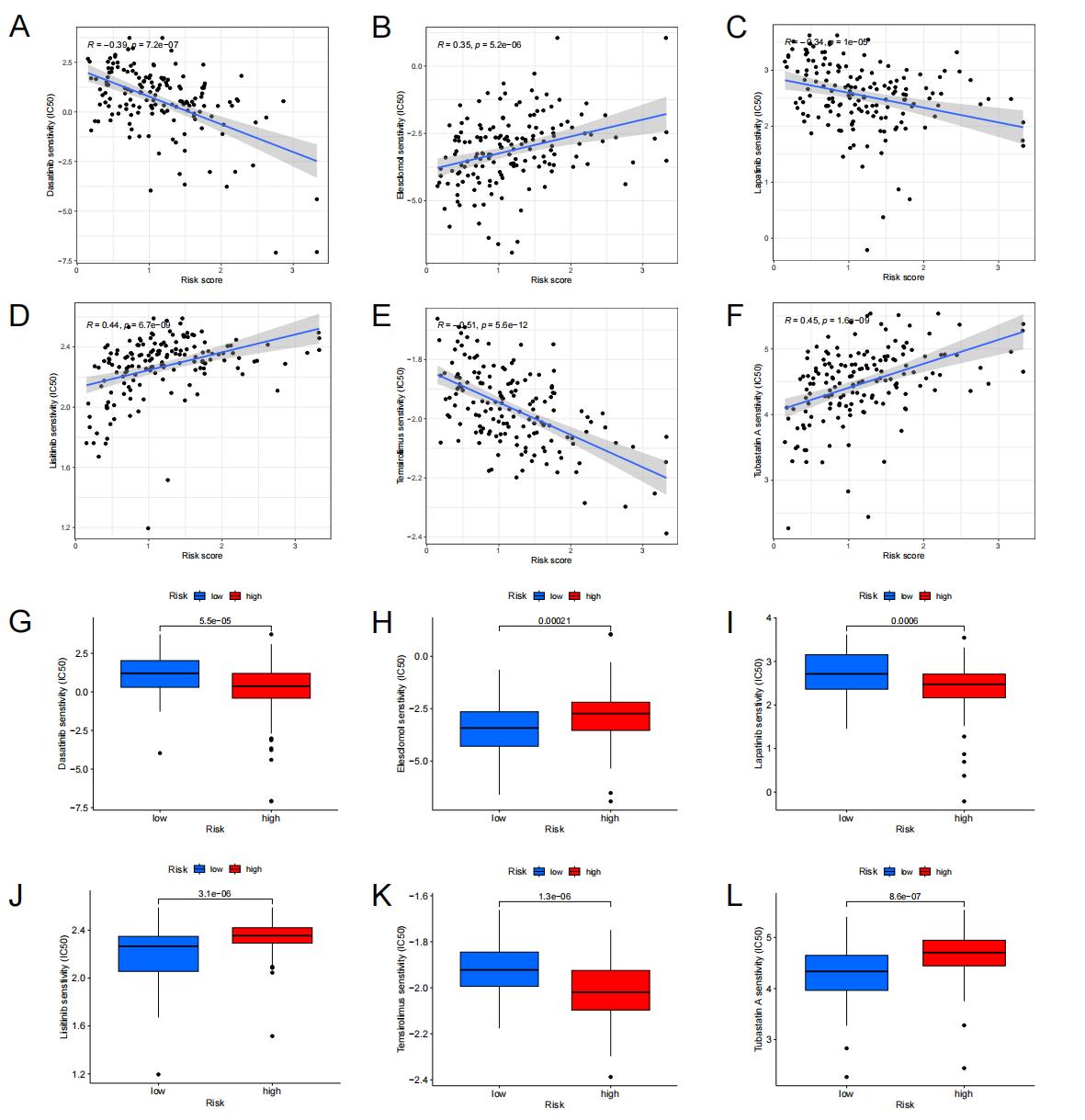
**Supplementary Fig. 1. Survival status and expression of RNF216P1 between high and low-risk groups.** (A-B) The expression of RNF216P1 and the relationship between riskScore and survival status. Survival regression analysis of high and low-risk group.



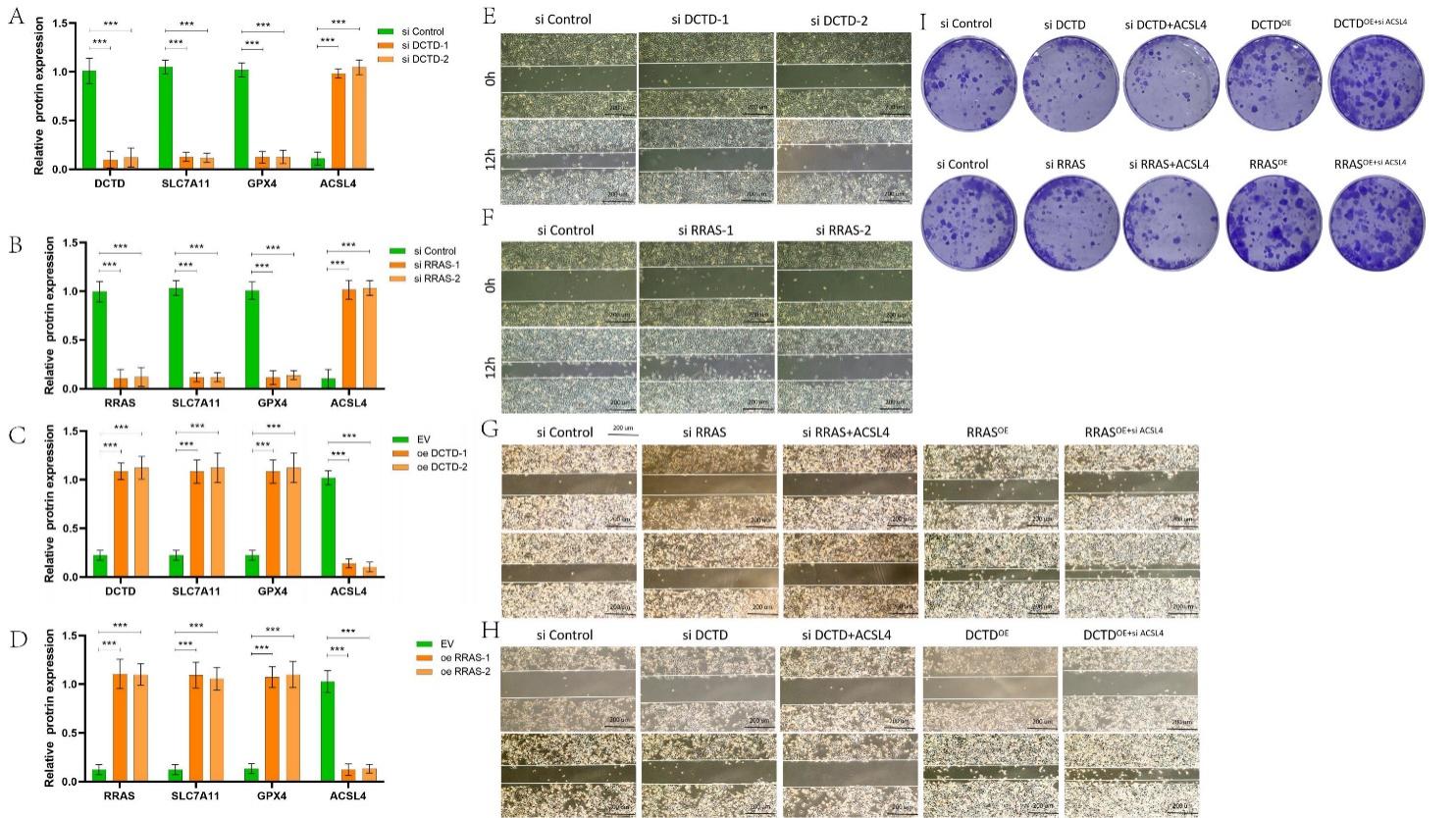
**Supplementary Fig. 2. Validation of risk regression model.**  ROC curve for riskScore, gender, and age.



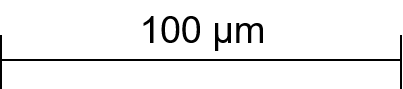
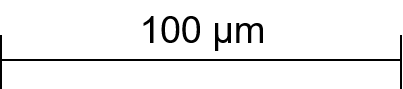
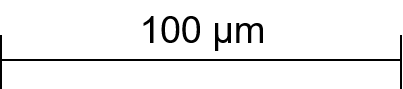
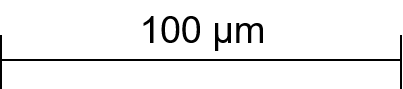
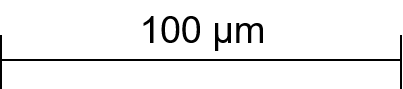
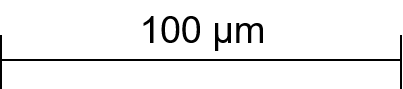
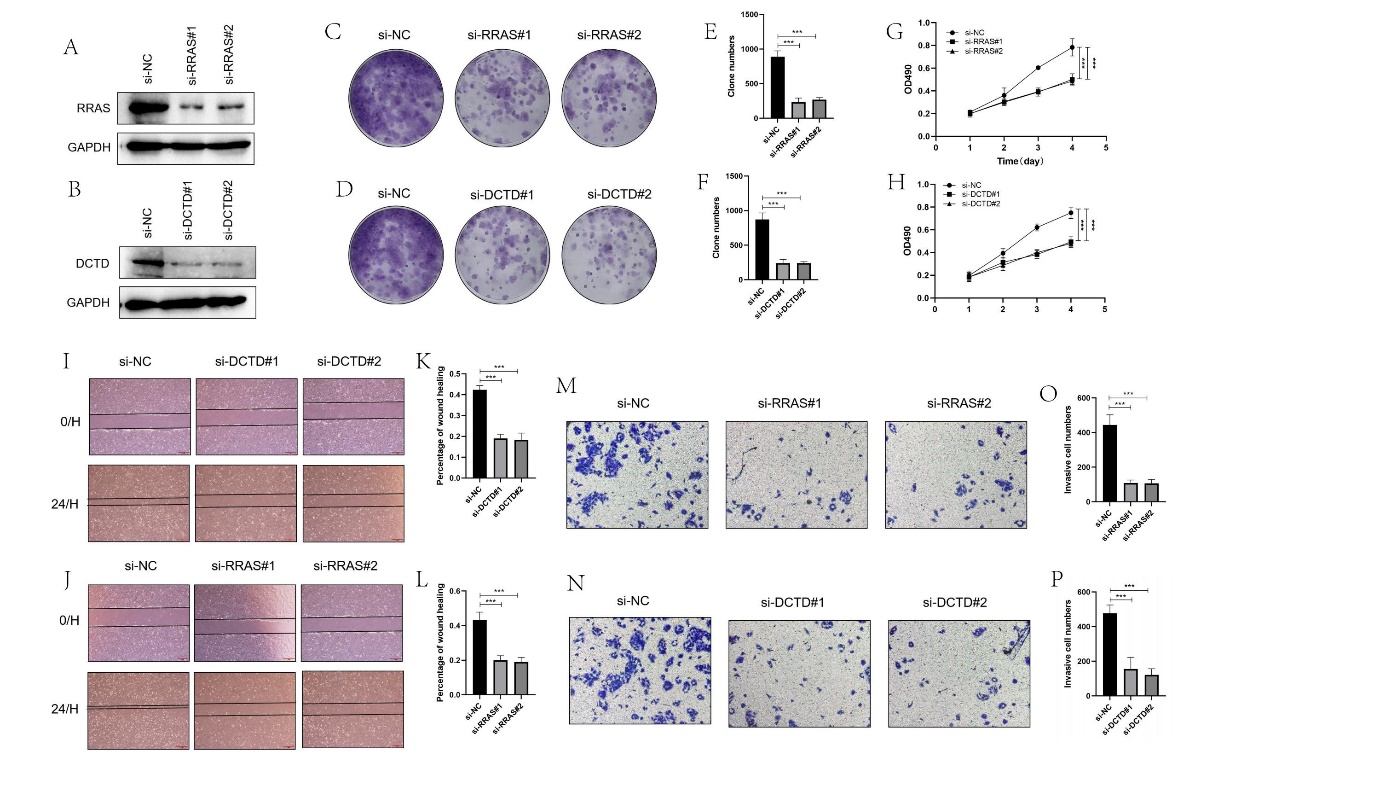
**Supplementary Fig. 3. Immunotherapy response between the high-risk and low-risk groups. \*\*p < 0.01; \*\*\*p < 0.001; ns > 0.05. (A-K) Immunotherapy response between the high-risk and low-risk groups (CAF, CD8, CD274, etc).**

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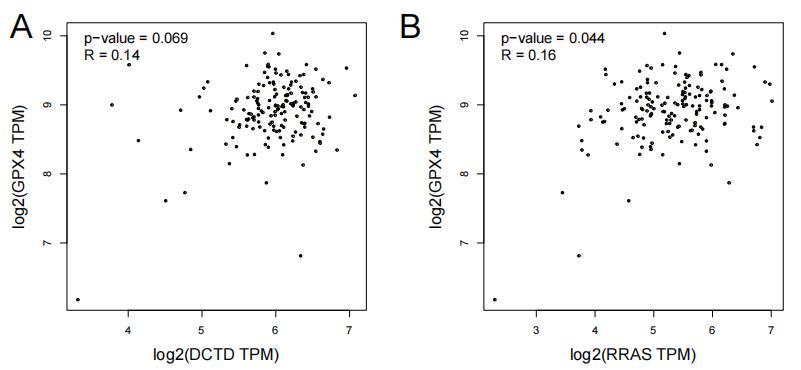
**Supplementary Fig. 4. The riskScore correlation with the IC50 values of elacridar, lestaurtinib, and tubastatin A.** (A-F) The riskScore correlation with the IC50 values of elacridar, lestaurtinib, and tubastatin A. (G-L) The IC50 values of elacridar, lestaurtinib, and tubastatin A in low risk group and high risk group.

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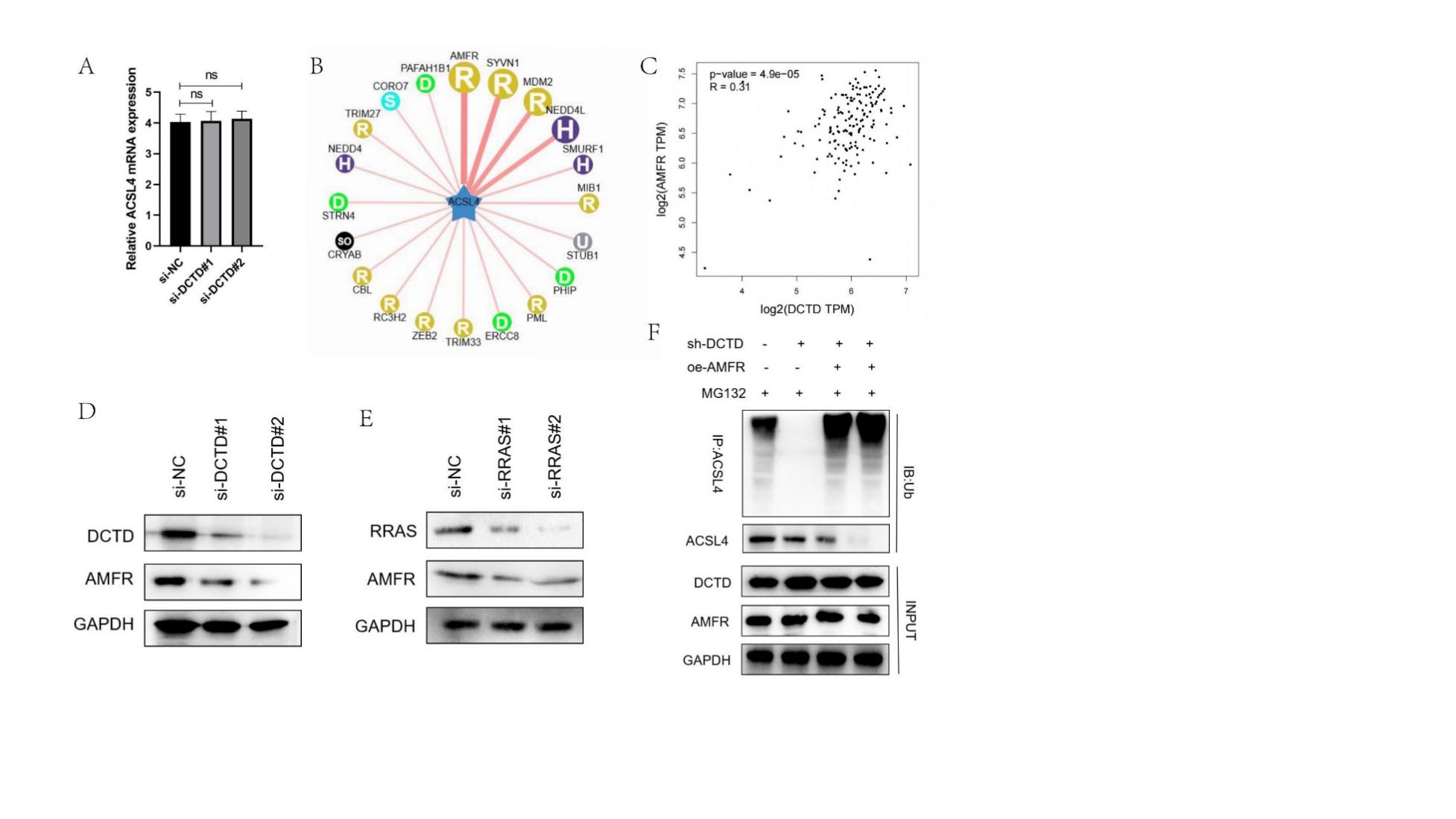
**Supplementary Fig. 5.** (A-D) Quantification of the Western blot results in Figure 11A-D. (E-F) are the images of Figure 10G-H with added scales. (G-H) Results of Figure 11I-K after adding scales and readjusting the annotation lines. (I) New cloning results obtained from repeated experiments of Figure 11E-G. Scale bar (100 µm). \*\*\*p < 0.001.



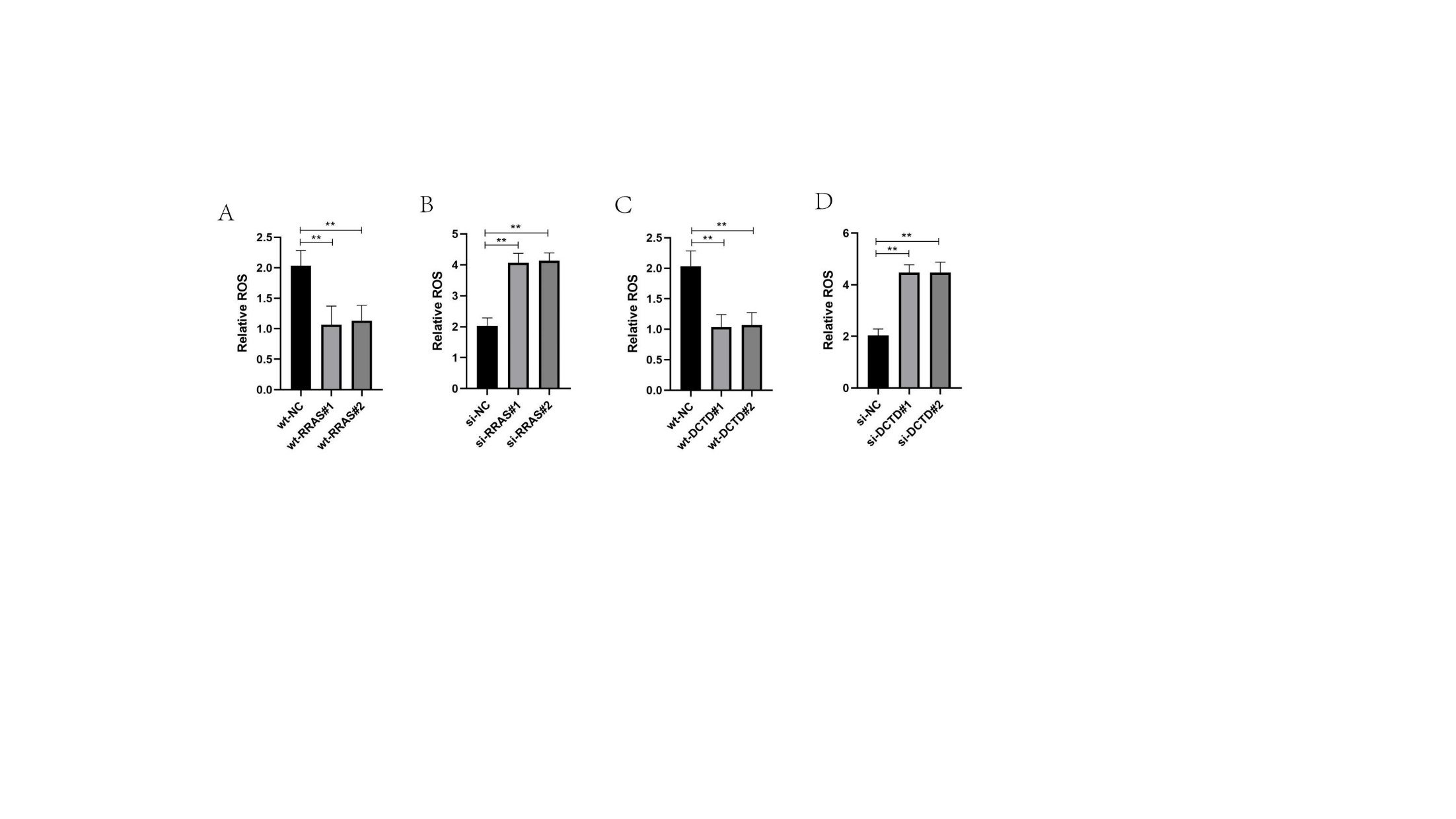
**Supplementary Fig. 6. DCTD and RRAS promote the proliferation, migration and invasion of GBM.** (A, B) Protein expression after DCTD or RRAS knockdown. (C-F) Clone formation experiment after DCTD or RRAS knockdown. (G, H) MTT experiment after DCTD or RRAS knockdown. (I-L) Wound healing test after DCTD or RRAS knockdown. Scale bar (200 µm) (M-P) Invasion Assay after DCTD or RRAS knockdown. Scale bar (100 µm) \*\*\*p < 0.001.



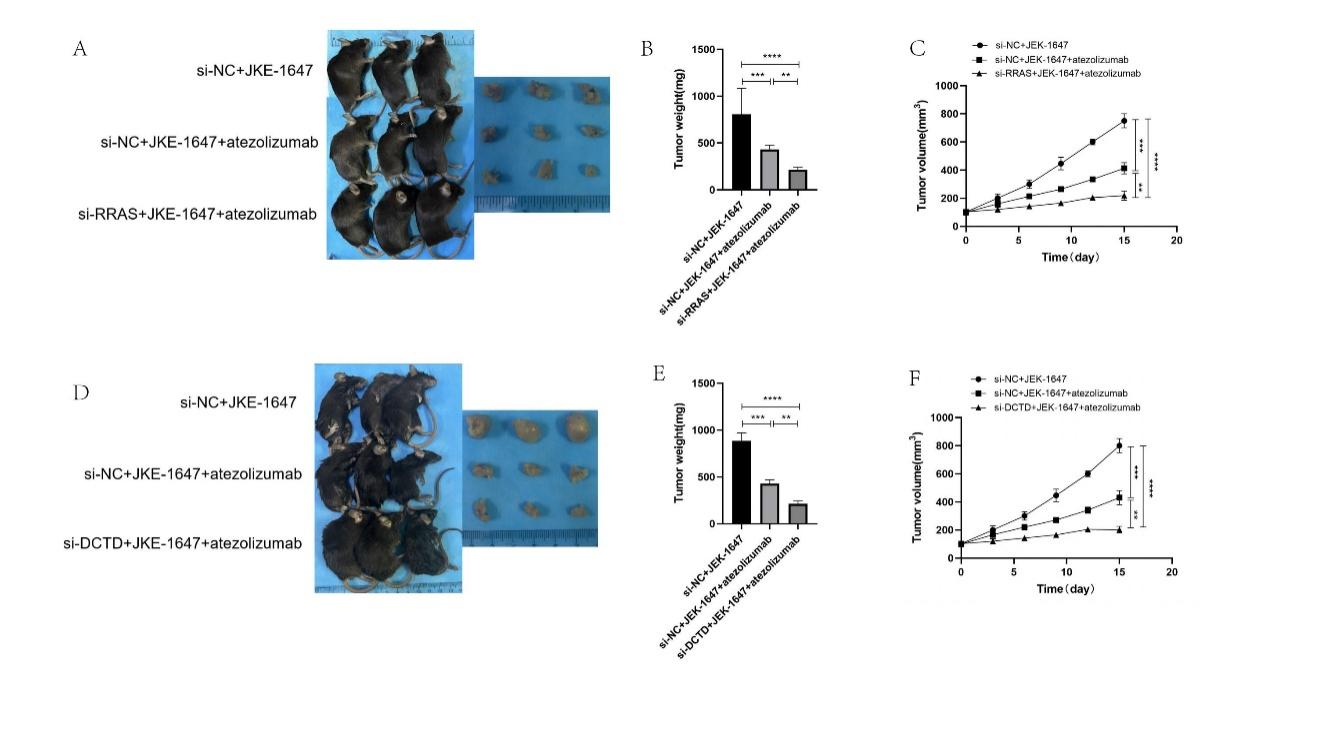
**Supplementary Fig. 7. The correlation of DCTD, RRAS, and GPX4.** GEPIA software shows the relationship between GPX4 and DCTD (A) and RRAS (B).

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**Supplementary Fig. 8. DCTD regulates ferroptosis by E3 ubiquitin ligases.** (A) RNA level of ACSL4 after DCTD knockdown. (B) Ubibrowser website identified AMFR as a regulator of ACSL4. (C) The correlation of DCTD and AMFR. (D-E) AMFR protein expression after DCTD or RRAS knockdown. (F) Ubiquitination level of ACSL4 after DCTD knockdown. ns > 0.05.



**Supplementary Fig. 9. DCTD and RRAS inhibit ROS level in GBM.** (A-B) ROS level after RRAS knockdown and overexpression. (C-D) ROS level after DCTD knockdown and overexpression. \*\*p < 0.01.



**Supplementary Fig. 10. Effect of JKE-1647 combined with atezolizumab on the growth of subcutaneous transplanted tumors in mice.** (A-C)CDX model construction and tumor volume and weight detection in RRAS knockdown groups. (D-F) CDX model construction and tumor volume and weight detection in DCTD knockdown groups. \*\*p < 0.01; \*\*\*p < 0.001; \*\*\*\*p < 0.0001.

**Supplementary Table 1. eQTL data from the IEU OpenGWAS project.**

**Supplementary Table 2. The risk coefficient of the scoring genes of riskScore.**

**Supplementary Table 3. 17,258 significant eQTLs and 56,706 genome-wide SNPs.**

**Supplementary Table 4. 15,306 eQTLs and 52,674 genome-wide SNPs.**

**Supplementary Table 5. 15,035 genes were retained for MR analysis.**

**Supplementary Table 6. The MR analysis results of 15,035 gene in GBM using 5 different methods.**

**Supplementary Table 7. The MR analysis results of 250 risk-related genes in GBM using IVW method.**

**Supplementary Tables 8. 9,942 differentially expressed genes associated with risk of GBM,**

**Supplementary Table 9. 50 genes significantly associated with GBM.**

**Supplementary Table 10. RiskScore for GBM patients.**

**Supplementary Table 11. A list of differentially expressed genes between high-risk and low-risk groups.**

**Supplementary Tables 12, 13. GO enrichment analysis in the high-risk and low-risk groups.**

**Supplementary Tables 14, 15. KEGG enrichment analysis in the high-risk and low-risk groups.**

**Supplementary Table 16. Immune infiltration analysis scores in GBM using 7 different methods.**

**Supplementary Table 17. The TIDE analysis results in GBM.**